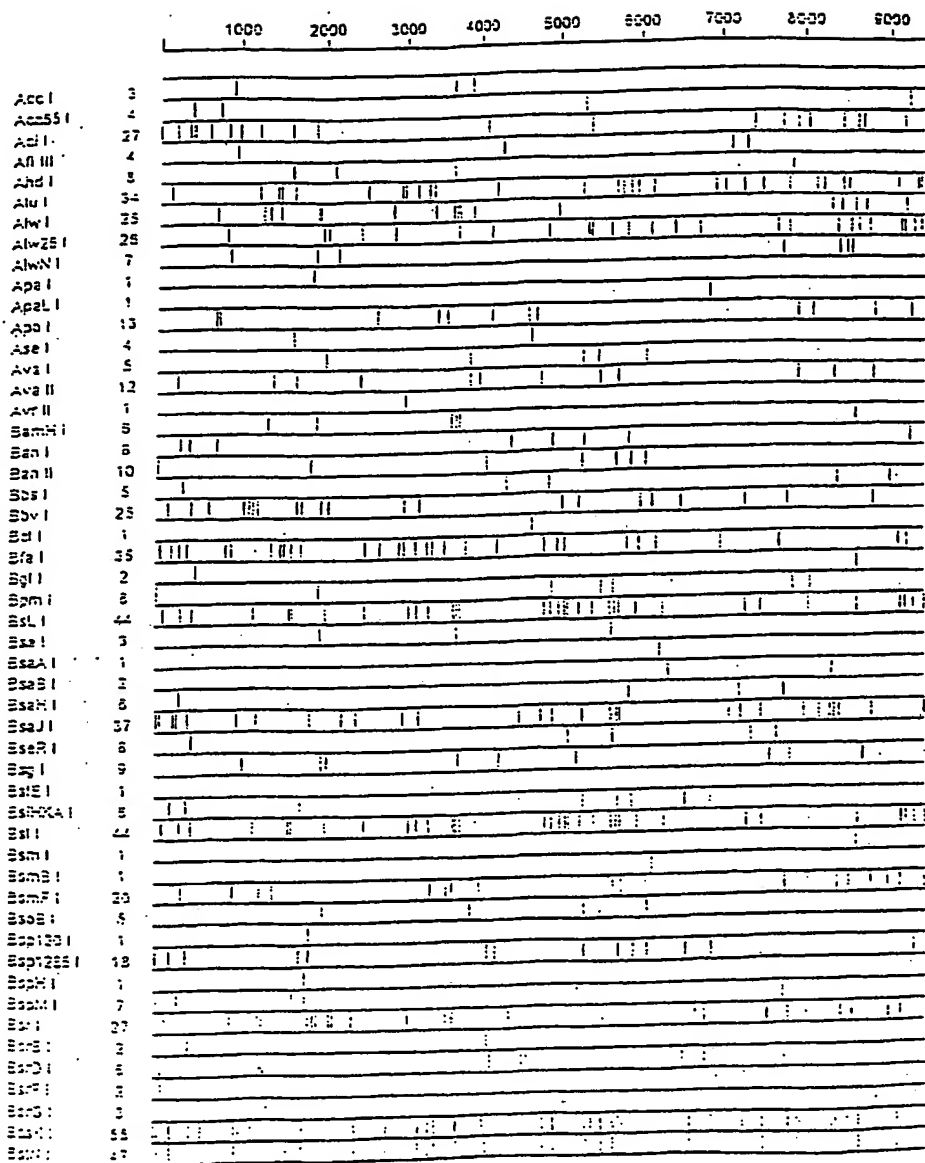


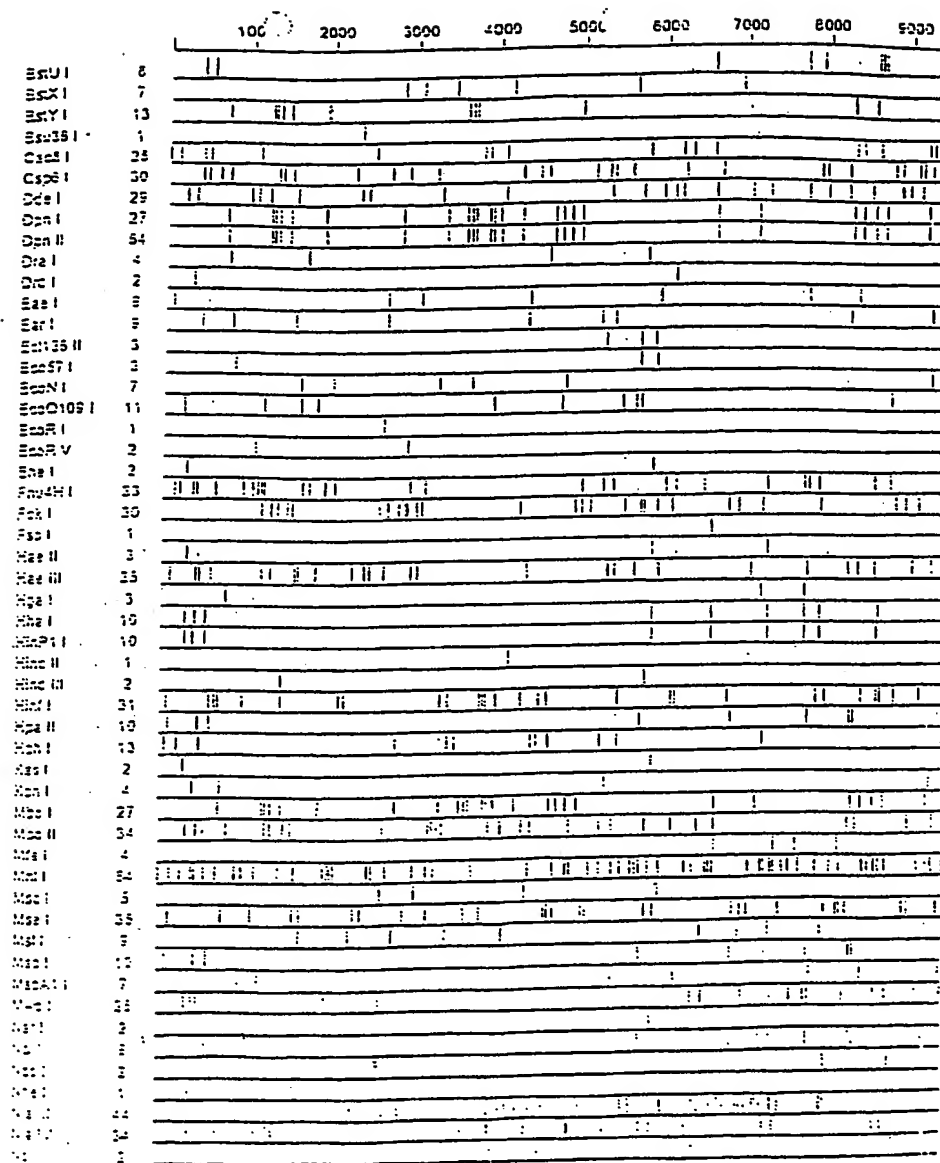
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FIG. 1A



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FIG. 1B



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FIG. 1C

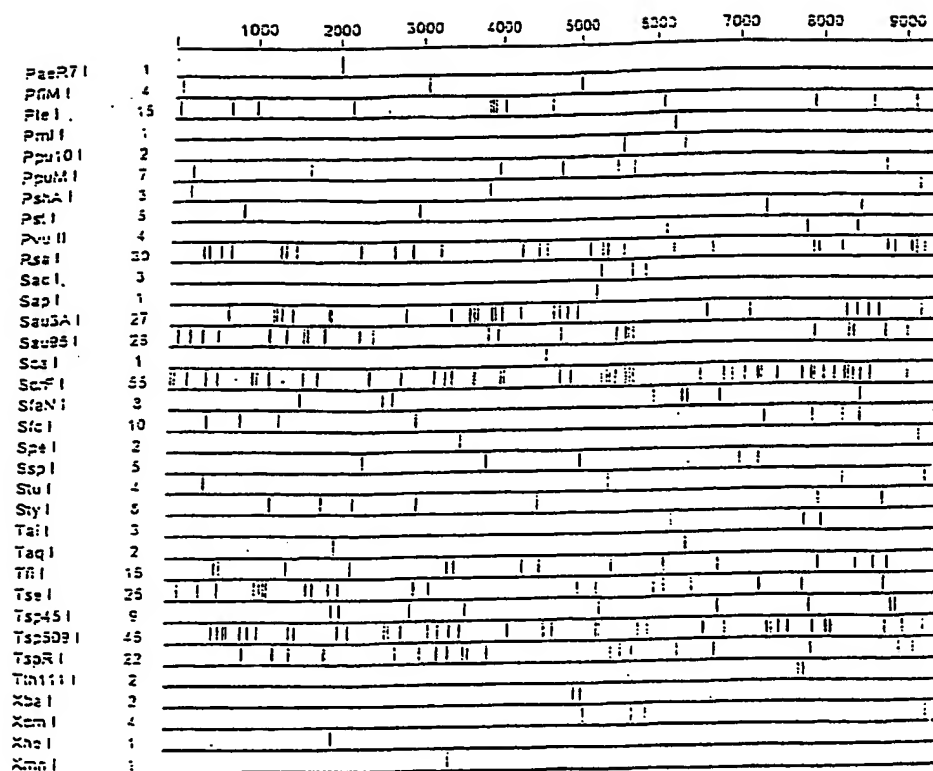
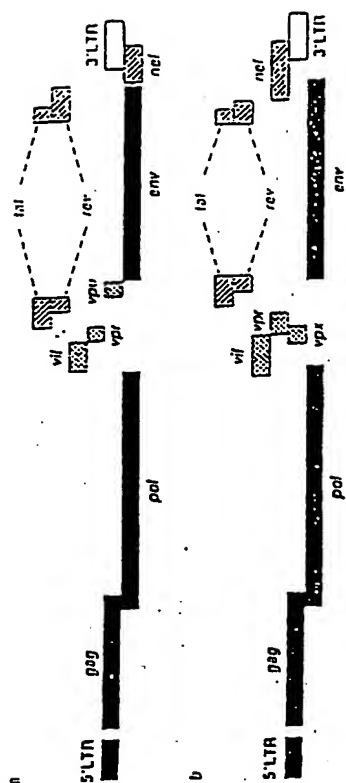


FIG. 2



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FIG. 3A
pROD(PK36) Leader Sequence

HIV2ROD ROD(PK36)	310 GTTGGCGCCT GTTGGCGCCT	320 GAACAGGGAC GAACAGGGAC	330 TTGAAGAAGA TTGAAGAAGA	340 CTGAGAAAGTC CTGAGAAAGTC	350 TTGGAACACG TTGGAACACG
HIV2ROD ROD(PK36)	360 GCTGAGTGAA GCTGAGTGAA	370 GGCAGTAAGG GGCAGTAAGG	380 GCGGCAGGAA GCGGCAGGAA	390 CAAACCACGA CAAACCACGA	400 CGGAGTGCTC CGGAGTGCTC
HIV2ROD ROD(PK36)	410 CTAGAAAGGC CTAGAAAGGC	420 GCGGGCCGAG GCGGGCCGAG	430 GTACCAAAGG GTACCAAAGG	440 CAGCGTGTGG CAGCGTGTGG	450 AGCGGGAGGA AGCGGGAGGA
HIV2ROD ROD(PK36)	460 GAAGAGGCCT GAAGAGGCCT	470 CCGGGTGAAG CCGGGTGAAG	480 GTAAGTACCT GTAAGTACCT	490 ACACCAAAAA ACACC	500 CTGTAGCCGA CTGTAGCCGA
HIV2ROD ROD(PK36)	510 AAGGGCTTGC	520 TATCCTACCT	530 TTAGACAGGT	540 AGAAGATTGT T	550 GGGAGATGGG GGGAGATGGG

FIG. 3B
pROD(SK36) Leader Sequence

HIV2ROD ROD(SK36)	310 GTTGGCGCCT GTTGG	320 GAACAGGGAC	330 TTGAAGAAGA	340 CTGAGAAAGTC	350 TTGGAACACG
HIV2ROD ROD(SK36)	360 GCTGAGTGAA	370 GGCAGTAAGG	380 GCGGCAGGAA	390 CAAACCACGA	400 CGGAGTGCTC
HIV2ROD ROD(SK36)	410 CTAGAAAGGC	420 GCGGGCCGAG	430 GTACCAAAGG	440 CAGCGTGTGG	450 AGCGGGAGGA
HIV2ROD ROD(SK36)	460 GAAGAGGCCT CT	470 CCGGGTGAAG CCGGGTGAAG	480 GTAAGTACCT GTAAGTACCT	490 ACACCAAAAA ACACCAAAAA	500 CTGTAGCCGA CTGTAGCCGA
HIV2ROD ROD(SK36)	510 AAGGGCTTGC AAGGGCTTGC	520 TATCCTACCT TATCCTACCT	530 TTAGACAGGT TTAGACAGGT	540 AGAAGATTGT AGAAGATTGT	550 GGGAGATGGG GGGAGATGGG

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FIG. 3C
pROD(SD36) Leader Sequence

HIV2ROD ROD(SD36)	310 GTTGGCGCCT	320 GAACAGGGAC	330 TTGAAGAAGA	340 CTGAGAAAGTC	350 TTGGAACACG
	GTTGG				
HIV2ROD ROD(SD36)	360 GCTGAGTGAA	370 GGCAGTAAGG	380 GCGGCAGGAA	390 CAAACCACGA	400 CGGAGTGCTC
HIV2ROD ROD(SD36)	410 CTAGAAAGGC	420 GCGGGCCGAG	430 GTACCAAAGG	440 CAGCGTGTGG	450 AGCGGGAGGA
HIV2ROD ROD(SD36)	460 GAAGAGGCCT	470 CCGGGTGAAG	480 GTAAGTACCT	490 ACACCAAAAA	500 CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACAC	
HIV2ROD ROD(SD36)	510 AAGGGCTTGC	520 TATCCTACCT	530 TTAGACAGGT	540 AGAAGATTGT	550 GGGAGATGGG
				GT	GGGAGATGGG

FIG. 3D
pROD(CG36) Leader Sequence

HIV2ROD ROD(CG36)	310 GTTGGCGCCT	320 GAACAGGGAC	330 TTGAAGAAGA	340 CTGAGAAAGTC	350 TTGGAACACG
	GTTGGCGCCT	GAACAGGGAC	TTGAAGAAGA	CTGAGAAAGTC	TTGGAACACG
HIV2ROD ROD(CG36)	360 GCTGAGTGAA	370 GGCAGTAAGG	380 GCGGCAGGAA	390 CAAACCACGA	400 CGGAGTGCTC
	GCTGAGTGAA	GGCAGTAAGG			
HIV2ROD ROD(CG36)	410 CTAGAAAGGC	420 GCGGGCCGAG	430 GTACCAAAGG	440 CAGCGTGTGG	450 AGCGGGAGGA
HIV2ROD ROD(CG36)	460 GAAGAGGCCT	470 CCGGGTGAAG	480 GTAAGTACCT	490 ACACCAAAAA	500 CTGTAGCCGA
	CT	CCGGGTGAAG	GTAAGTACCT	ACACC	
HIV2ROD ROD(CG36)	510 AAGGGCTTGC	520 TATCCTACCT	530 TTAGACAGGT	540 AGAAGATTGT	550 GGGAGATGGG
				GT	GGGAGATGGG

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FIG. 3E
pROD(MR36) Leader Sequence

HIV2ROD ROD(MR36)	310 GTTGGCGCCT GTTGG	320 GAACAGGGAC	330 TTGAAAGAAGA	340 CTGAGAAGTC	350 TTGGAACACG
HIV2ROD ROD(MR36)	360 GCTGAGTGAA	370 GGCAGTAAGG	380 GCGGCAGGAA GCGGCAGGAA	390 CAAACCACGA CAAACCACGA	400 CGGAGTGCTC CGGAGTGCTC
HIV2ROD ROD(MR36)	410 CTAGAAAGGC CTAGAAAGGC	420 GCGGGCCGAG GCGGGCCGAG	430 GTACCAAAGG GTACCAAAGG	440 CAGCGTGTGG GAGCGTGTGG	450 AGCGGGAGGA AGCGGGAGGA
HIV2ROD ROD(MR36)	460 GAAGAGGCCT GAAAGAGGCT	470 CCGGGTGAAG CCGGGTGAAG	480 GTAAGTACCT GTAAGTACCT	490 ACACCAAAAA ACACC	500 CTGTAGCCGA
HIV2ROD ROD(MR36)	510 AAGGGCTTGC	520 TATCCTACCT	530 TTAGACAGGT	540 AGAAGATTGT GT	550 GGGAGATGGG GGGAGATGGG

FIG. 4A

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HIV-2 pROD(SD36/EM) Sequence of Mutant Region of Envelope
(Insertion mutant)

ROD (6351)	ACAGAGGCTT TTGATGCAT	
EM	ACAGAGGCTT TTGATGCATA GGTAGCGTGA GATCTTAGTG CA	
ROD		G GAATAATA CA (6380)
EM	TAGGTAGC CTCAGATCTT AGTGCAAAGA TCGAATAATA CA.	

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FIG. 4B

pCM-ENV(ROD)(B-14)

← ENV IE Plasmid →

```

1   TCAATATTGG CCATTAGCCA TATTATTCTT TGGTTATATA GCATAAATCA
51  ATATTGGCTA TTGGCCATTG CATACGTTGT ATCTATATCA TAATATGTAC
101 ATTTATATTG GCTCATGTCC AATATGACCG CCATGTTGGC ATTGATTATT
151 GACTAGTTAT TAATAGTAAT CAATTACGGG GTCATTAGTT CATAGCCCAT
201 ATATGGAGTT CCGCGTTACA TAACCTACGG TAAATGGCCC GCCTGGCTGA
251 CCGCCCAACG ACCCCCGCCC ATTGACGTCA ATAATGACGT ATGTTCCCAT
301 AGTACGCCCA ATAGGGACTT TCCATTGACC TCAATGGGTG GAGTATTAC
351 GGTAAACTGC CCACCTGGCA GTACATCAAG TGTATCATAT GCCAAGTCCG
401 CCCCCTATTG ACGTCAATGA CGGTAAATGG CCGCGCTGGC ATTATGCCCA
451 GTACATGACC TTACGGGACT TTCTTACTTG GCAGTACATC TACGTATTAG
501 TCATCGCTAT TACCATGGTG ATGCGGTTTT GGCAGTACAC CAATGGGCGT
551 GGATAGCGGT TTGACTCAGC GGGATTTCCA AGTCTCCACC CCATTGACGT
601 CAATGGGAGT TTGTTTGGC ACCAAAATCA ACGGGACTTT CCAAAATGTC
651 GTAATAACCC CGCCCCGTTG ACGCAAATGG CCGGTAGGCG TGTACGGTGG
701 GAGGTCTATA TAAGCAGAGC TCGTTTAGTG AACCGTCAGA TCACTAGAG
751 CTTTATTGCG GTACTTTATC ACAGTTAAAT TGCTAACGCA GTCAGTCTT
801 CTGACACCAAC AGTCTCGAAC TTAAGCTGCA GAAGTTGGTC GTGAGGCACT
851 GGGCAGGTAA GTATCAAGGT TACAAGACAG GTTTAAGGAG ACCAATAGAA
901 ACTGGGGCTG TCGAGACAGA GAAGACTCTT GCGTTTCTGA TAGGCACCTA
951 TTGGTCTTAC TGACATCCAC TTTGCTTTTC TCTCCACAGG TGTCACCTCC
1001 CAGTTCAATT ACAGCTCTTA AGGCTAGAGT ACTTAATACG ACTCACTATA
1051 GGTAGGCTC C5  TACACCAGAC AAGTGAGTAT 180
GATGAATCAG CTGCTTATTG CCATTTTATT AGCTAGTGCT TGCTTAGTAT ATTGCACCCA 240
ATATGTAACT GTTTTCTATG CGGTACCCAC GTGCAAAAAT GCAACCATTC CCTCTTTTT 300
310      320      330      340      350      360
TGCAACCAGA AATAGGGATA CTGGGGGAAC CATACAGTGC TTGCTGACA ATGATGATTA 380
TCAGGAAATA ACTTTGAATG TAACAGAGGC TTTTGATGEA TGGAAATAA CACTAAEAGA 420
ACAAGCAATG AAAGATGTET GGCATGTATT CGAGACATEA ATAAAACCAT GTGTCAAACT 480
AACACCTTTA TGTGTAGCAA TGAAATGCCAG CAGCACAGAG AGCAGCATAG GGAACAACAC 540
AACCTCAAAAG AGCACAAGCA CAACCCACAAC CACACCCACA GAECAGGAGC AAGGGGTGG 600
610      620      630      640      650      660
tgaggatcat ccatgggccc gggggggccc atgctcggg ttgggggggg cgggggggg 680
ccattggcag ttccatctga cgggattgga cggggctcgg ccccccocgt atctggccc 720
atggtactcc cggggtgttg ttgtgggccc ccttcctcga ccccggtttt 780
cctggcccat tggcccccat cggctcttcc cggctctcgt gggggggcct atgggggtg 840
tctggggttt agatcctgtg ccccccgggg ttatggcttc ttgggtgtg atgtacccc 900

```

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FIG. 4C

910	920	930	940	950	960
tttttcaggc	tttgccccc	actgtttctc	agttagtagt	tctccatgca	ccaggetget
ggcccccggc	acttccocat	ggtttggttt	tactggcact	agggcagaga	atagaccctc
tctctattgg	catggcagag	atantagacc	tctctcscgc	ttaccacact	attctctctc
cagtttgcat	tgtacggggc	cagggaccca	gatagtgaca	caaatcatgc	ttctgtcagg
ccatgtgttt	cactcccat	ccagccgat	cactccacgc	cccgaccacg	catgtgtctg
1210	1220	1230	1240	1250	1260
gttcccccgc	caatggcccg	acgccatgca	ggaggtagag	gacccacttg	ccccccatcc
caggctctgc	ggcccccctg	acccccggca	tattagcttt	gagcgccacg	gacccaggctc
agcccccagc	gtggcatcca	tgtggaccca	ctgcaggggc	gagtttctct	catgcacact
gacattggtt	ctccattggc	tggggaccca	gaccccccgc	cattatgccc	cgtcccatct
ccagcccatc	attccacact	ggcatcagg	agggcgccat	gtatatttgc	ctccacgggc
1510	1520	1530	1540	1550	1560
agggggagtg	tcttgccact	ccccgggccc	cagctcattt	gctccacttg	catggccccc
ccctctcccg	acccacattc	ccctttagtc	aggggtggcc	gacatctcca	ggttggagtt
ggggagttct	caattggtag	ccctacccc	cattgggttc	gaccccccac	agggcccccg
ctctctctct	gttccggggc	gacatccccc	aggtgtgttc	gtgttagggg	ttttgggttt
tctggccccc	gaggggtctg	ccctgggggc	gggttccctg	ccctgttcgg	ctccgtcccg
1810	1820	1830	1840	1850	1860
gcatttctct	gacgggagtg	tcccgccccc	gacccagctg	ttggccgttg	tcaggccccc
cccccgcctg	ttggccctgc	cagtttgggg	acggccccc	ctccggggcc	ggttcccttc
tctggggggc	tccctccagg	cccgggggcg	gctccatttc	ttgggggttg	cgttttagcc
agtcggccc	ccctctgttc	cattgggttc	gtattcttc	gacatgcat	ggcccccctt
gggtggggcg	gattggggcc	cccccgttcg	ctccctgggg	gacccctcca	gtcccccgtt
2110	2120	2130	2140	2150	2160
agcccccggc	cccttccagc	acggggccccc	tctgtatgca	ctcccccact	tccttagctg
gggtattttt	ggcccttggg	ttgacttccc	ctctgggttc	agttctcttc	actatggggg
gatttctctc	gtggcagtc	tggatttccg	actatgcttc	tctgtatgca	ccctgttccg
tgggttgggc	aggggtcttc	ggcctgtttt	ctcttccccc	cccggttctc	tcctcccgat
cccttctccc	ccggcccccgg	gacggccccc	cccccggggc	cccgccgggg	acgggtggccg
2410	2420	2430	2440	2450	2460
cccccggggc	gacgggtact	ggcccttggc	gatagcttat	ATACATTTC	TGATCCGCCA
GGTGATTGGC	CTCTTGACCA	GACTATACAG	CATCTGCAGG	GACTTACTAT	GCAGGACCTT
CTTGACCTTC	CAACTCATCT	ACCAGATCT	CAGAGACTGG	CTGAGACTTA	GAACAGCCCT
CTTGCAATAT	GGTCCGACT	GGATCCAGGA	AGCATTCGAG	GGCCCGCCGA	GGGCTACAGG
AGAGCTCTT	GGCCCGCCCT	GGAGCGGCTT	GTGAGCGCTA	TGGAGCCGAA	TGGGAGCGCG
2710	2720	2730	2740	2750	2760
ATGACTCCCG	GTTCAGGAA	GGATCAGAG	GGGAGGAGAA	ATGGCTCTCT	GTGAGCGAGG
GGATATATCC	CAAGGAGGCT	GTATGATATC	TCTCTTGG		

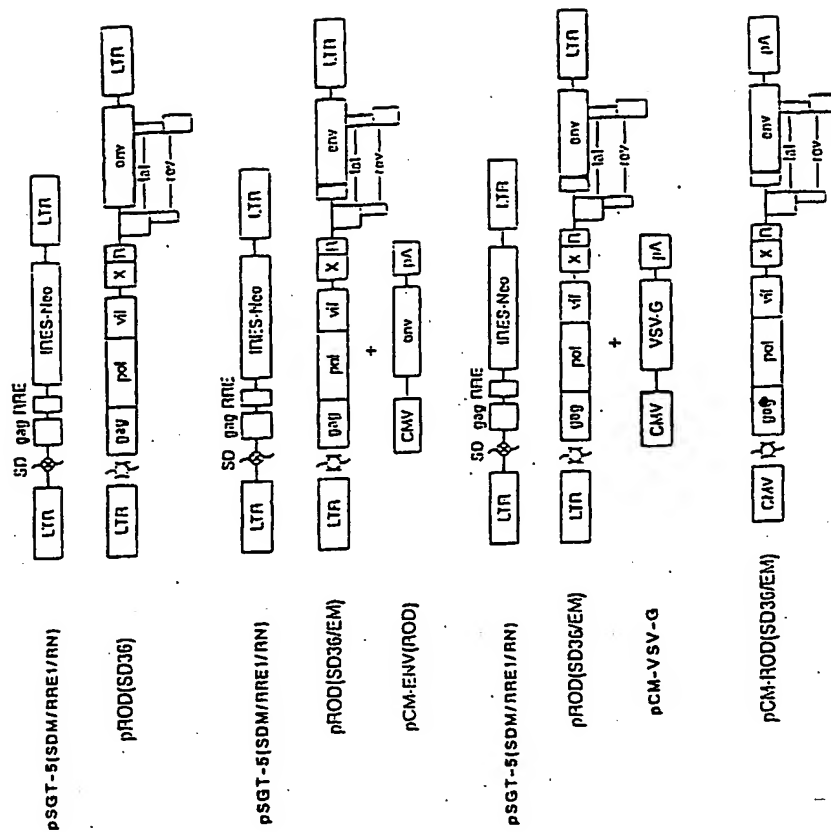
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FIG. 4D

→ ~~CAGGCGAG GGGGGGCTGG GGGGCACTGG GGGGGCGG~~ SV40 PA-
SV40 PA-
1101 CCGCTTCGAG CAGACATGAT AAGATACATT GATGAGTTTG GACAAACCAC
1151 AACTAGAATG CAGTGA AAAA AATGCTTTAT TTGTCAAATT TGTGATGCTA
1201 TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT TAACAACAAC
1251 AATTGCATTC ATTTTATGTT TCAGGTTTAC GGGGAGATGT GGGAGCTTTT
1301 TTAAGCAAG TAAACCTCT ACAAATGTGG TAAATCGAT AAGGATCCCG
1351 GCTGGCGTAA TAGCGAAGAG GCCCGCACCG ATCGCCCTTC CCAACAGTTG
1401 CGCAGCCTGA ATGCCCAATG CAGCGGCCCT GTAGCGGCGG ATTAAGCGCG
1451 GCGGGTGTGG TGGTTACGGG CAGCGTGACC GCTACACTTG CCAGCGCCCT
1501 AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC CTTTCTCGCC ACGTTTCGGG
1551 CTTTCCCCG TCAAGCTCTA AATCGGGGCG TCCCTTTAGG GTTCCGATT

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FIG. 4E HIV-2 Vector System: Native and Pseudotype



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FIG. 5A

SIV 5' LTR Leader Sequence

```

R-
      10      20      30      40      50
GCTCTGTATT CAGTCGCTCT GCGGAGAGGC TGGCAGATTG AGCCCTGGGA
      60      70      80      90     100
GGTTCTCTCC AGCACTAGCA GGTAGAGCCT GGGTGTTCCT TCCTAGACTC
      110     120     130     140     150
TCACCAGCAC TTGGCCGGTG CTGGGCAGAG TGACTCCACG CTTGCTTGCT
                                - R[US]-
      160     170     180     190     200
TAAAGCCCTC TTCAATAAAG CTGCCATTTT AGAAGTAAGC TAGTGTGTGT
      210     220     230     240     250
TCCCATCTCT CCTAGCCGCC GCCTGGTCAA CTCGGTACTC AATAATAAGA
      260     270     280     290     300
AGACCCTGGT CTGTTAGGAC CCTTTCTGCT TTGGGAAACC GAAGCAGGAA
      310     320     330     340     350
- US [Leader]-
AATCCCTAGC AGATTGGCGC CTGAACAGGG ACTTGAAGGA GAGTGAGAGA
      360     370     380     390     400
CTCCTGAGTA CGGCTGAGTG AAGGCAGTAA GGGCGGCAGG AACCAACCAC
      410     420     430     440     450
GACGGAGTGC TCCTATAAAG GCGCGGGTCC GTACCAGACG GCGTGAGGAG
      460     470     480     490     500
CGGGAGAGGA AGAGGCCTCC GGTTCAGGT AAGTCAACA CAAAAAGAA
      510     520     530     540     550
ATACCTGTCT TTTATCCAGG AAGGGGTAAT AAGATAGAGT GGGAGATGGG
      560
CGTGAGAAAC

```

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FIG. 5B

pSIV(SD36)

WTL	320	330	340	350	360
SD36	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	GATTGG				
WTL	370	380	390	400	410
SD36	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
WTL	420	430	440	450	460
SD36	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCCTGAGGAG	CGGGAGAGGA
WTL		SD			
SD36	470	480	490	500	510
	AGAGGCCTCC	GTTTGCAGGT	AAGTCCAACA	CAAAAAAGAA	ATAGCTGTCT
	CTCC	GTTTGCAGGT	AAGTCCAACA	CA	
WTL	520	530	540	550	560
SD36	TTTATCCAGG	AAGGGGTAAT	AAGATAGACT	GGGAGATGGG	CGTGAGAAAC
			GT	GGGAGATGGG	CGTGAGAAAC

FIG. 5C

pSIV(SDM)

WTL	320	330	340	350	360
SDM	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
	GATTGGCGC	CTGAACAGGG	ACTTGAAGGA	GAGTGAGAGA	CTCCTGAGTA
WTL	370	380	390	400	410
SDM	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACCAACCAC	GACGGAGTGC
WTL	420	430	440	450	460
SDM	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCCTGAGGAG	CGGGAGAGGA
	TCCTATAAAG	GCGCGGGTCG	GTACCAGACG	GCCTGAGGAG	CGGGAGAGGA
WTL		SD			
SDM	470	480	490	500	510
	AGAGGCCTCC	GTTTGCAGGT	AAGTCCAACA	CAAAAAAGAA	ATAGCTGTCT
	AGAGGCCTCC	GTTTGCAGGT	AAGTCCAACA	CAAAAAAGAA	ATAGCTGTCT
WTL	520	530	540	550	560
SDM	TTTATCCAGG	AAGGGGTAAT	AAGATAGACT	GGGAGATGGG	CGTGAGAAAC
	TTTATCCAGG	AAGGGGTAAT	AAGATAGACT	GGGAGATGGG	CGTGAGAAAC

FIG. 6A

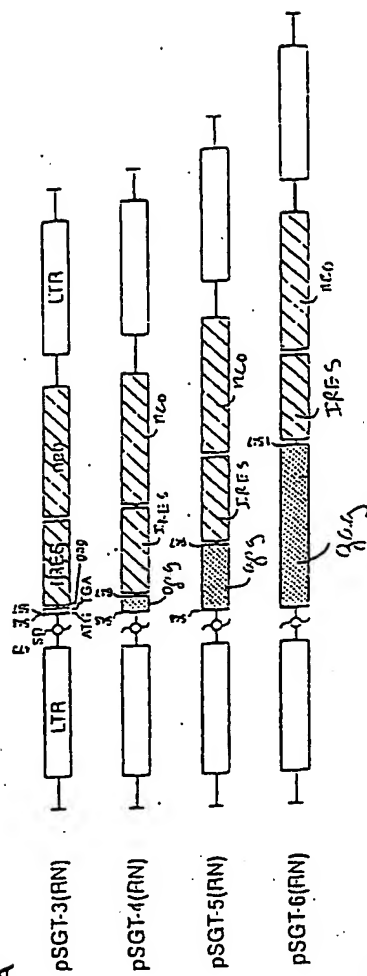
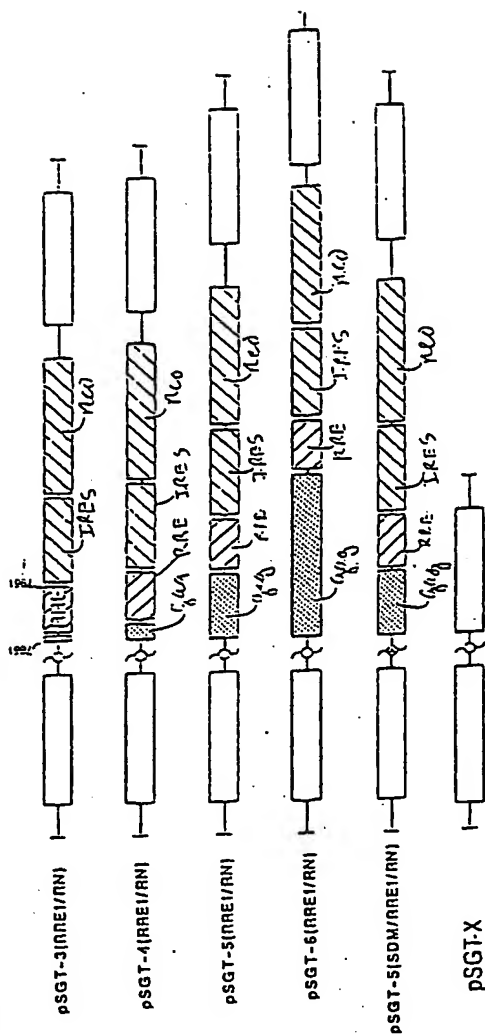


FIG. 6B



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FIG. 7A

U3	530	520			
GGAA	GGGCTGTATT	ACAGTGATAG			
-530	-520	-510	-500	-490	-480
GAGACGTAGA	GTCTAGACA	TATACTTAGA	AAAGGAAGAG	GGAATAATTG	GAGACTGGCA
-470	-460	-450	-440	-430	-420
GAACATACT	CATG GACCAG	GAGTAAGGTA	TCCAAAGTTC	TTGGGTGGT	TATGGAAGCT
-410	-400	-390	-380	-370	-360
AGTACCAGTA	GATGTCCAC	AAGA GGGAGA	TGACAGTGAG	ACTCACTGCT	TAGTGCATCC
-350	-340	-330	-320	-310	-300
AGCA CAAACA	AGCAGGTTTG	ATGACCCGCA	TGGAGAAACA	TTAGTTTGGA	GGTTTGACCC
-290	-280	-270	-260	-250	-240
CACGCTAGCT	TTTAGCTACG	AGGCCTTTAT	TCGATACCCA	GAGGAGTTTG	GGTACAAGTC
-230	-220	-210	-200	-190	-180
AGGCCTGCCA	GAGGATGAAT	GGAAGGCAAG	ACTGAAAGCA	AGAGGGATAC	CGTTAGCTA
-170	-160	-150	-140	-130	-120
AAAACAGGAA	CAGCTATACT	TGGTCAGGGC	AGGAAGTAAC	TAACAGAAAA	CAGCTGAGAC
-110	-100	-90	-80	-70	-60
TGCAGGGACT	TTCCAGAAGG	GGCTGTTACC	AGGGGAGGGA	CATGGGAGGA	GCCGGTGGGG
-50	-40	-30	-20	-10	U3
AACGCCCTCA	TACTTTCTGT	ATAAATGTAC	CCGCTACTCG	CATTGTATTC	
R	10	20	30	40	50
GTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA	GCACTAGCAG
70	80	90	100	110	120
TGGTCACCTG	GGTGTTCCT	GCTAGACTCT	CACCAGTGCT	TGGCCGGCAC	TGGGCAGACG
130	140	150	160	170	R U5 180
GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA
190	200	210	220	230	240
GTGTGTGCTC	CCATCTCTCC	TAGTCGCCGC	CTGGTCATTG	GGTGTTCATC	TAAAGTAACA
250	260	270	280	290	300
AGACCCTGGT	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
U5 Leader 310	320	330	340	350	360
AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA	CGGCTGAGTG
370	380	390	400	410	420
AAGGCAGTAA	GGGCGGCAGG	AACAAAACAC	GACGGAGTGC	TCCTAGAAAA	GCGCAGGCCG

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FIG. 7B

430	440	450	460	470 —SDM—	480
AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG	TGAAAGAGGC	CTCCGGGTGA	TATCAGTGCC
490	500	510	520	530	540
TACACCAAAT	ACAGTAGCCA	GAAGGGCTTG	TTATCCTACC	TTTAGACGGG	TAGAAGATTG
Leader gag	560	570	580	590	600
TGGGAGATGC	CATGGTAGGG	CGCGAGAAAC	TCCGTCTTGA	GAGGGAAAAA	AGCAGACGAA
610	620	630	640	650	660
TTAGAAAAGA	TTAGGTTACG	GCCCGGCGGA	AAGAAAAAAT	ATAGGCTAAA	ACATATTGTG
670	680	690	700	710	720
TGGGCAGCGA	ATGAATTGGA	CAGATTCGGA	TTGGCAGAGA	GCCTGTTGGA	GTCAAAAGAG
730	740	750	760	770	780
GGTTGCCAAAA	AAATTCTTAC	AGTTTTAGAT	CCATTAGTAC	CGACAGGGTC	AGAAAAATTA
790	800	810	820	830	840
AAAAGCCTTT	TTAATACTGT	CTGCGTCATT	TGGTGTATAC	ACGCAGAAGA	GAAAGCGAAA
850	860	870	880	890	900
GATACTGAAG	AAGCAAAACA	AAAGGTACAG	AGACATCTAG	TGGCAGAAAC	AAAAACTACA
910	920	930	940	950	gag(955) poly(L)
GAAAAAATGC	CAAGTACAAG	TAGACCAACA	GCACCACCTA	GCGGGAACGG	AGGAACTCGA
970	980	RRE(7661) 990	1000	1010	1020
ATGCTGGTGT	ACCGCGGCCG	CAGAGGTGTA	TTCGTGCTAG	GGTTCTTAGG	TTTTCTCACA
1030	1040	1050	1060	1070	1080
GCAGGAGCTG	CAATGGGCGC	GGCGTCCTTG	ACGCTGTCCG	CTCAGTCTCG	GACTTTATTG
1090	1100	1110	1120	1130	1140
GCCGGGATAG	TGCAGCAACA	GCAACAGCTG	TTGGACGTGG	TCAAGAGACA	ACAAGAAATG
1150	1160	1170	1180	1190	1200
TTGCCACTGA	CCGTCTGGGG	AACAAAAAAT	CTCCAGGCAA	GAGTCACTGC	TATCGAGAAA
1210	1220	1230	1240	1250	1260
TACTTAAAGG	ACCAGGCGC	AACTAAATTCA	TGGGGATGTG	CGTCTAGACA	AGTCTGCCAC
1270	RRE(7960) poly(L)	1290	(8770)	1310	1320
ACTACTGTAC	CATGGGTAGC	GGCCGCTCGC	GAGTAGACCA	TGGAGAGCCC	CAGCAGAAGG
1330	1340	1350	1360	1370	1380
GGAGAAAGGC	TCGTACAAGC	AACAAAATAT	GGATGATGTA	GATTCAGATG	ATGATGACCT
1390	1400	1410	1420	1430	1440
AGTAGGGGTC	CCTGTCACAC	CAAGAGTACC	ATTAAGAGAA	ATGACATATA	GGTTGGCAAG
1450	1460	1470	(8944) U3 1480	1490	1500
AGAT ATGTCA	CATTTGATAA	AAGAAAAGGG	GGGACTGGAA	GGGCTGTATT	ACAGTGATAG

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FIG. 7C

1510 GAGACGTAGA	1520 GTCCTAGACA	1530 TATACTTAGA	1540 AAAGGAAGAG	1550 GGAATAATTG	1560 GAGACTGGCA
1570 GAACTATACT	1580 CATG GACCAG	1590 GAGTAAGGTA	1600 TCCAAAGTTC	1610 TTTGGGTGGT	1620 TATGGAAGCT
1630 AGTACCAGTA	1640 GATGTCCAC	1650 AAGA GGGAGA	1660 TGACAGTGAG	1670 ACTCACTGCT	1680 TAGTGCATCC
1690 AGCA CAAACA	1700 AGCAGGTTTG	1710 ATGACCCGCA	1720 TGGAGAAACA	1730 TTAGTITGGA	1740 GGTTTGACCC
1750 CACGCTAGCT	1760 TTTAGCTACG	1770 AGGCCTTTAT	1780 TCGATACCCA	1790 GAGGAGTTTG	1800 GGTACAAGTC
1810 AGGCCTGCCA	1820 GAGGATGAAT	1830 GGAAGGCAAG	1840 ACTGAAAGCA	1850 AGAGGGATAC	1860 CGTTAGCTA
1870 AAAACAGGAA	1880 CAGCTATACT	1890 TGGTCAGGGC	1900 AGGAAGTAAC	1910 TAACAGAAAA	1920 CAGCTGAGAC
1930 TGCAGGGACT	1940 TTCCAGAAGG	1950 GGCTGTTACC	1960 AGGGGAGGGA	1970 CATGGGAGGA	1980 GCCGGTGGGG
1990 AACGCCCTCA	2000 TACTTTCTGT	2010 ATAAATGTAC	2020 CCGCTACTCG	U3 R CATTGTATTG	2040 AGTCGCTCTG
2050 CGGAGAGGCT	2060 GGCAGATTGA	2070 GCCC TGGGAG	2080 GTTCTCTCCA	2090 GCACTAGCAG	2100 GTAGGCCTG
2110 GGTGTTCCT	2120 GCTAGACTCT	2130 CACCAGTGCT	2140 TGGCCGGCAC	2150 TGGGCAGACG	2160 GCTCCACGCT
2170 TGCTTGCTTA	2180 AAAGACCTCT	2190 TAATAAAGC	R TGCCA		

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FIG. 7D

10 20 30 40 50 60
TCTAGAGGAA TTCCGCCCTT CTCCCTCCCC CCCCCCTAAC GTTACTGGCC GAAGCCGCTT
70 80 90 100 110 120
GGAATAAGGC CGGTGTGCGT TTGCTATAT GTTATTTTCC ACCATATTGC CGTCTTTTGG
130 140 150 160 170 180
CAATGTGAGG GCCCGGAAAC CTGGCCCTGT CTTCTTGACC AGCATTCTTA GGGGTCTTTC
190 200 210 220 230 240
CCCTCTCCCC AAGCAATGC AAGGTCTGTT GAATCTGCTG AAGGAAGCAG TTCCTCTGGA
250 260 270 280 290 300
AGCTTCTTGA AGACAAACAA CGTCTGTACC GACCCTTTGC AGGCAGCGGA ACCCCCCACC
310 320 330 340 350 360
TGGCGACAGG TCCCTCTGCG GCCAAAGGCC ACGTCTATAA GATACACCTC CAAAGGCGGC
370 380 390 400 410 420
ACAACCCAG TCCACCGTTC TGAGTTGGAT AGTTGTGGA AGAGTCAAT GGCTCTCCTC
430 440 450 460 470 480
AAGCCTATT AACAAGGGGC TGAAGGATGC CCAGAAGGTA CCCCATTGTA TGGGATCTGA
490 500 510 520 530 540
TCTGGGSCCT CGGTGCACAT GCTTTACATG TGTTTAGTGG AGGTTAAAA ACCTCTAGGC
550 560 570 580 590 600
CCCCCGAACC ACGGGGACGT GGTTCCTT TGA AAAACAC GATGATAAG TTGCCACAAC
610 620 630 640 650 660
CATGGCTGAA CAAGATCGAT TGCACGCAGG TTCTCCGGCC GCTTGGGTGG AGAGGCTATT
670 680 690 700 710 720
CGGCTATGAC TGGGCACAA AGACAATCGG CTGCTCTGAT GCCCGCGGT TCCGGCTGTC
730 740 750 760 770 780
AGCGCAGGGG CCCCCGCTT TTTTGTCAA GACCGACCTG TCCGGTGCCC TGAATGAAT
790 800 810 820 830 840
GCAGGACGAG GCAGCGCGGC TATCGTGGCT GGCCACGACG GGCCTTCCTT CCCCACCTGT
850 860 870 880 890 900
GCTCGACGTT CTCACGAG CGGGAAGGGA CTGGCTGCTA TTGGGCGAAG TGCCGGCGCA
910 920 930 940 950 960
GGATCTCCTG TCATCTCACC TTGCTCCTGC CGAGAAAGTA TCCATCATGG CTGATGCAAT
970 980 990 1000 1010 1020
GCGGCGGCTG CATACCCCTT ATCCGGCTAC CTGCCCCATT CACCACCAAG CGAATCATCG
1030 1040 1050 1060 1070 1080
CATCGAGCGA GCACCTACTC GGATGGAAGC CGCTCTTCTC GATCAGGATG ATCTGGACGA
1090 1100 1110 1120 1130 1140
AGAGCATCAC GGGCTCGGCG CAGCCGAAC CTTCGCCAGC CTCAGGCGCG GCATCCCCGA
1150 1160 1170 1180 1190 1200
CGGCGAGGAT CTCGTGCTGA CCCATGGCGA TGCCTGCTTG CCGAATATCA TGGTGGAAAA
1210 1220 1230 1240 1250 1260
TGGCGGCTTT TCTCGATTCA TCGACTGTGG CCGGCTGGCT GTGGCGGAGC GGTATGAGTA
1270 1280 1290 1300 1310 1320
CATAGCGCTG CCTACCCCTG ATATTGCTGA AGAGCTTGGC GCGCAATGGG CTGACCGCTT
1330 1340 1350 1360 1370 1380
CCTCTGCTT TACGCTATCG CCGCTCCCGA TTGCGACGCG ATCGGCTTCT ATCGGCTTCT
1390 1400 1410
TGACGAGTTC TTCTGAGCGG GATCGGCTAG C

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FIG. 7E

pSGT-5(SDM) 5'LTR-Leader Sequence

HIV2ST pSGT5(SDM)	10 GTTTCGCTCTG	20 CGGAGAGGCT	30 GGCAGATTGA	40 GCCCTGGGAG	50 GTTCTCTCCA
	GTTTCGCTCTG	CGGAGAGGCT	GGCAGATTGA	GCCCTGGGAG	GTTCTCTCCA
HIV2ST pSGT5(SDM)	60 GCACTAGCAG	70 TGGTCACCTG	80 GGTGTTCCT	90 GCTAGACTCT	100 CACCAGTGCT
	GCACTAGCAG	TGGTCACCTG	GGTGTTCCT	GCTAGACTCT	CACCAGTGCT
HIV2ST pSGT5(SDM)	110 TGGCCGGCAC	120 TGGGCAGACG	130 GCTCCACGCT	140 TGCTTGCTTA	150 AAAGACCTCT
	TGGCCGGCAC	TGGGCAGACG	GCTCCACGCT	TGCTTGCTTA	AAAGACCTCT
HIV2ST pSGT5(SDM)	160 TAATAAAGCT	170 GCCAGTTAGA	180 AGCAAGTTAA	190 GTGTGTGCTC	200 CCATCTCTCC
	TAATAAAGCT	GCCAGTTAGA	AGCAAGTTAA	GTGTGTGCTC	CCATCTCTCC
HIV2ST pSGT5(SDM)	210 TAGTCGCCGC	220 CTGGTCATTG	230 GGTGTTCATC	240 TAAAGTAACA	250 AGACCCTGGT
	TAGTCGCCGC	CTGGTCATTG	GGTGTTCATC	TAAAGTAACA	AGACCCTGGT
HIV2ST pSGT5(SDM)	260 CTGTTAGGAC	270 CCTTTCTGCT	280 TTGGGAAACC	290 AAGGCAGGAA	300 AATCCCTAGC
	CTGTTAGGAC	CCTTTCTGCT	TTGGGAAACC	AAGGCAGGAA	AATCCCTAGC
HIV2ST pSGT5(SDM)	310 AGGTTGGCGC	320 CCGAACAGGG	330 ACTTGAAGAA	340 GACTGAGAAG	350 CCTTGGAACA
	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
HIV2ST pSGT5(SDM)	360 CGGCTGAGTG	370 AAGGCAGTAA	380 GGCGGGCAGG	390 AACAAACCAC	400 GACGGAGTGC
	CGGCTGAGTG	AAGGCAGTAA	GGCGGGCAGG	AACAAACCAC	GACGGAGTGC
HIV2ST pSGT5(SDM)	410 TCCTAGAAAA	420 GCGCAGGCCG	430 AGGTACCAAG	440 GGCGGCGTGT	450 GGAGCGGGAG
	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
HIV2ST pSGT5(SDM)	460 TGAAAGAGGC	470 CTCCGGGTGA	480 AGGTAAGTGC	490 CTACACCAAA	500 TACAGTAGCC
	TGAAAGAGGC	CTCCGGGTGA	TATCACTGC	CTACACCAAA	TACAGTAGCC
HIV2ST pSGT5(SDM)	510 AGAAGGGCTT	520 GTTATCCTAC	530 CTTTAGACGG	540 GTAGAAGATT	550 GTGGAGATG
	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGAGATG

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FIG. 7F

pSGT-5(SDM) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDM)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDM)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDM)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
		SD			
	460	470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDM)	TGAAAGAGGC	CTCCGGGTGA	TATCAGTGC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDM)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

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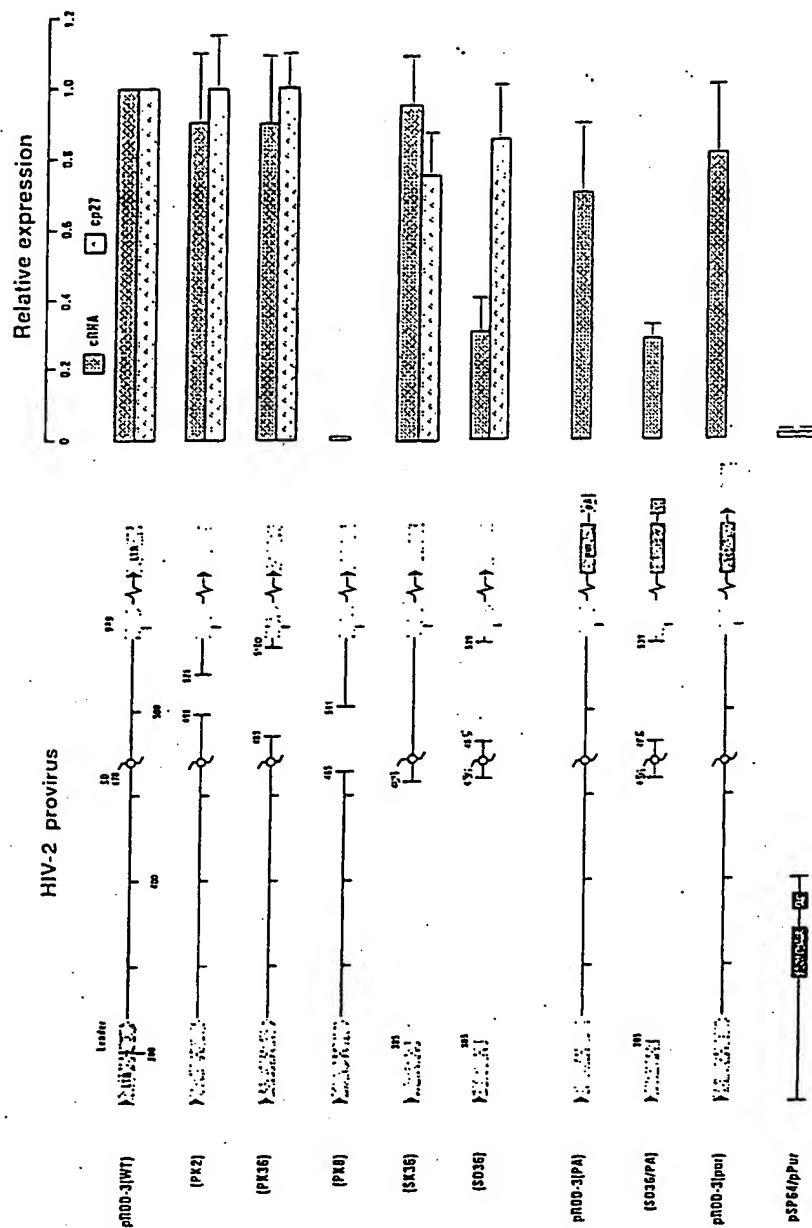
FIG. 7G

pSGT-5(SDX) Leader Sequence

	310	320	330	340	350
HIV2ST	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
pSGT5(SDX)	AGGTTGGCGC	CCGAACAGGG	ACTTGAAGAA	GACTGAGAAG	CCTTGGAACA
	360	370	380	390	400
HIV2ST	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
pSGT5(SDX)	CGGCTGAGTG	AAGGCAGTAA	GGGCGGCAGG	AACAAACCAC	GACGGAGTGC
	410	420	430	440	450
HIV2ST	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
pSGT5(SDX)	TCCTAGAAAA	GCGCAGGCCG	AGGTACCAAG	GGCGGCGTGT	GGAGCGGGAG
	460	SD 470	480	490	500
HIV2ST	TGAAAGAGGC	CTCCGGGTGA	AGGTAAGTGC	CTACACCAAA	TACAGTAGCC
pSGT5(SDX)	TGAAAGAGGC	CTCCGG	GC	CTACACCAAA	TACAGTAGCC
	510	520	530	540	550
HIV2ST	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGGGAGATG
pSGT5(SDX)	AGAAGGGCTT	GTTATCCTAC	CTTTAGACGG	GTAGAAGATT	GTGG AGATG

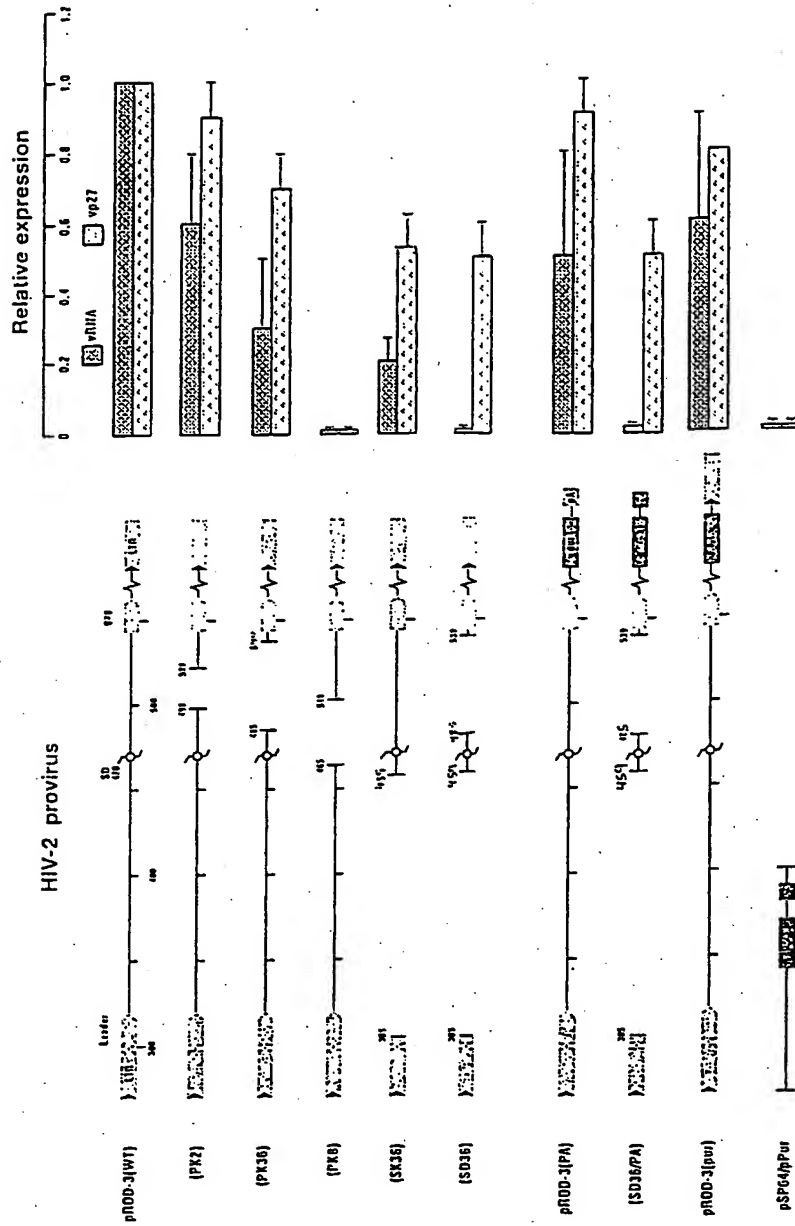
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FIG. 8



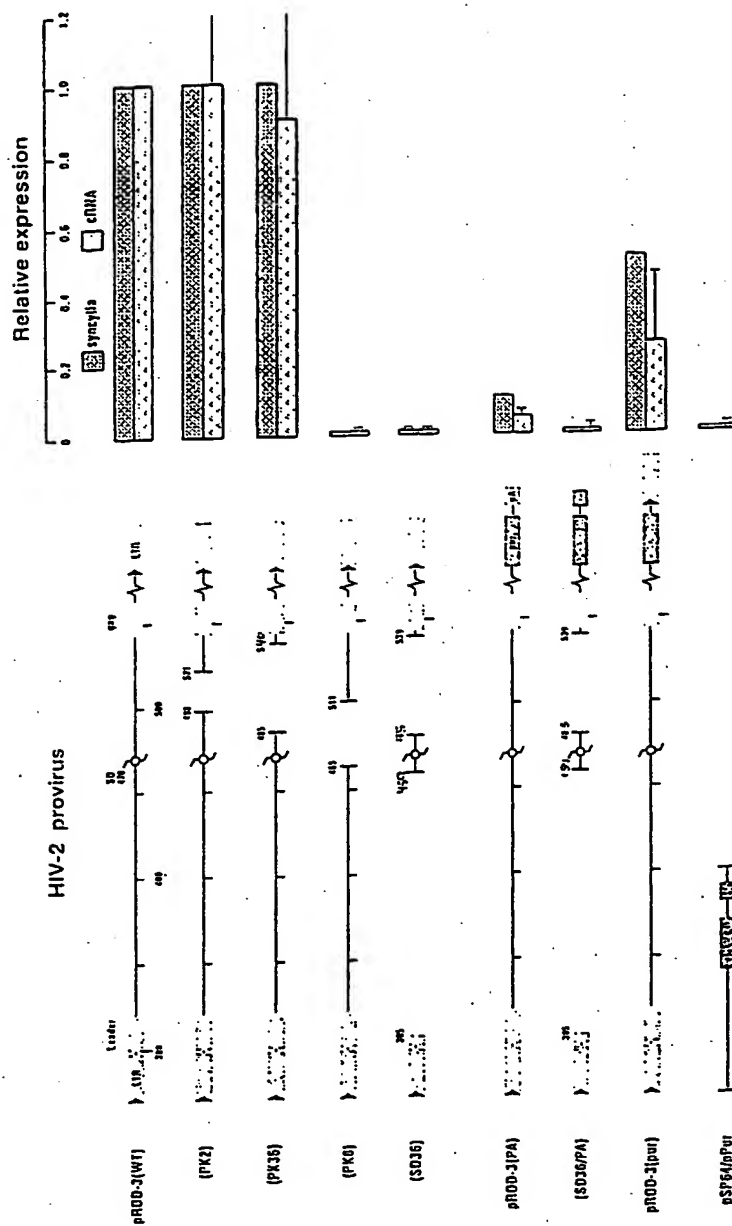
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FIG. 9



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FIG. 10



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FIG. 11

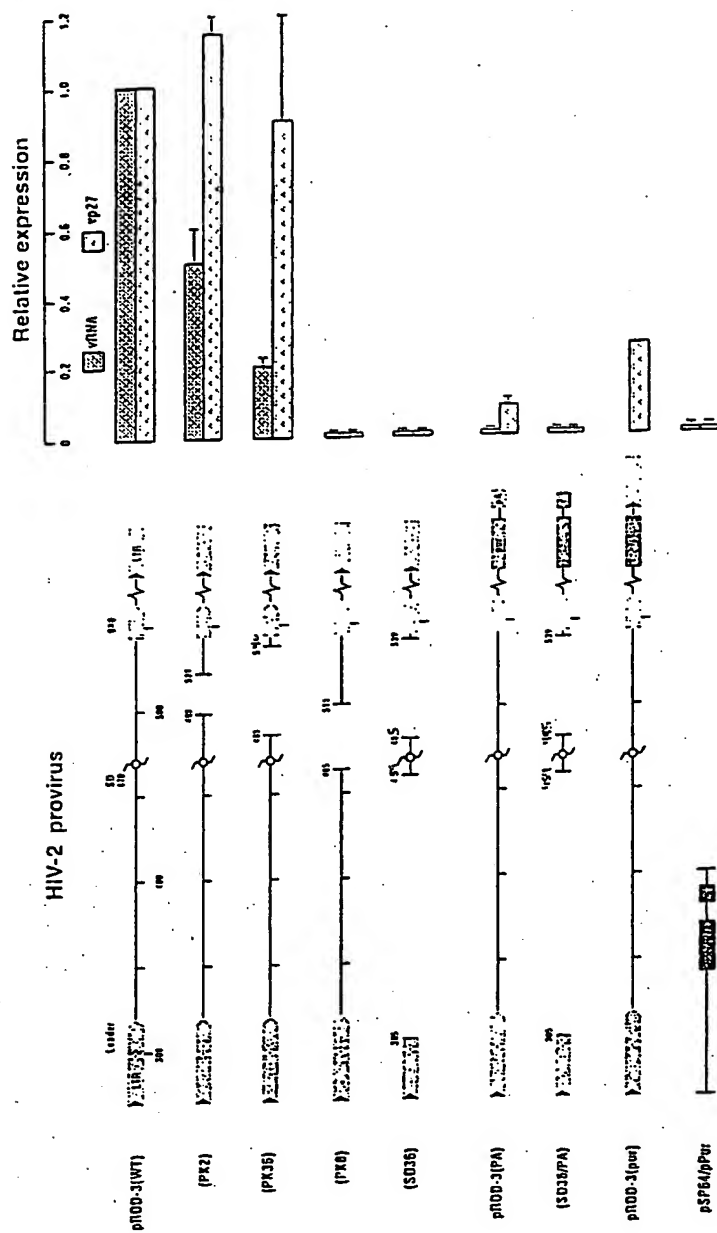


FIG. 12

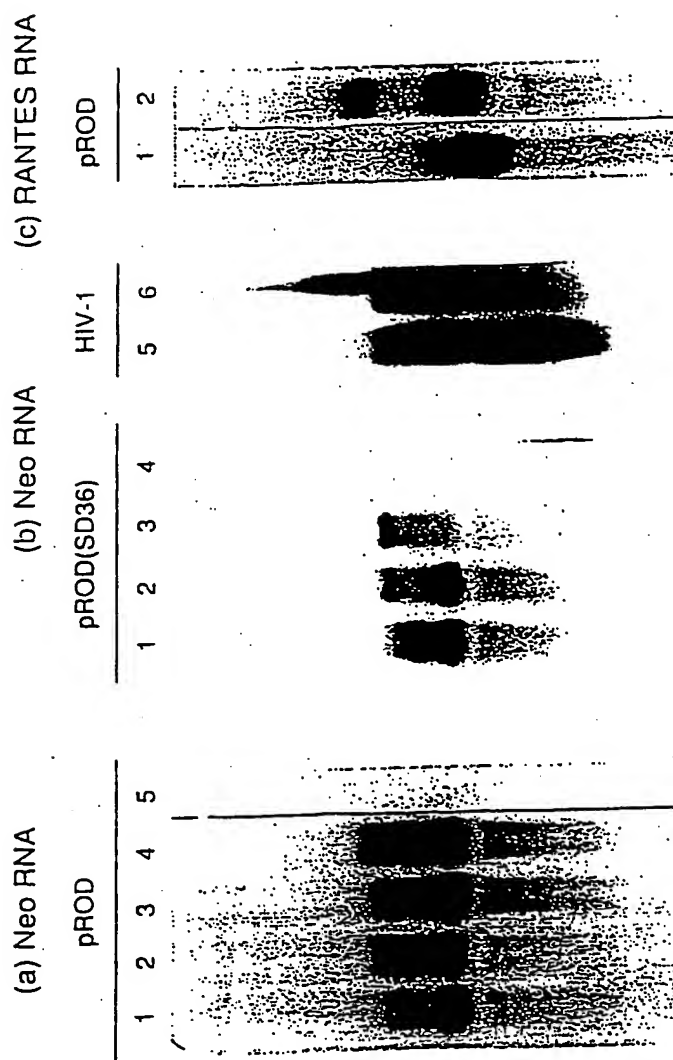
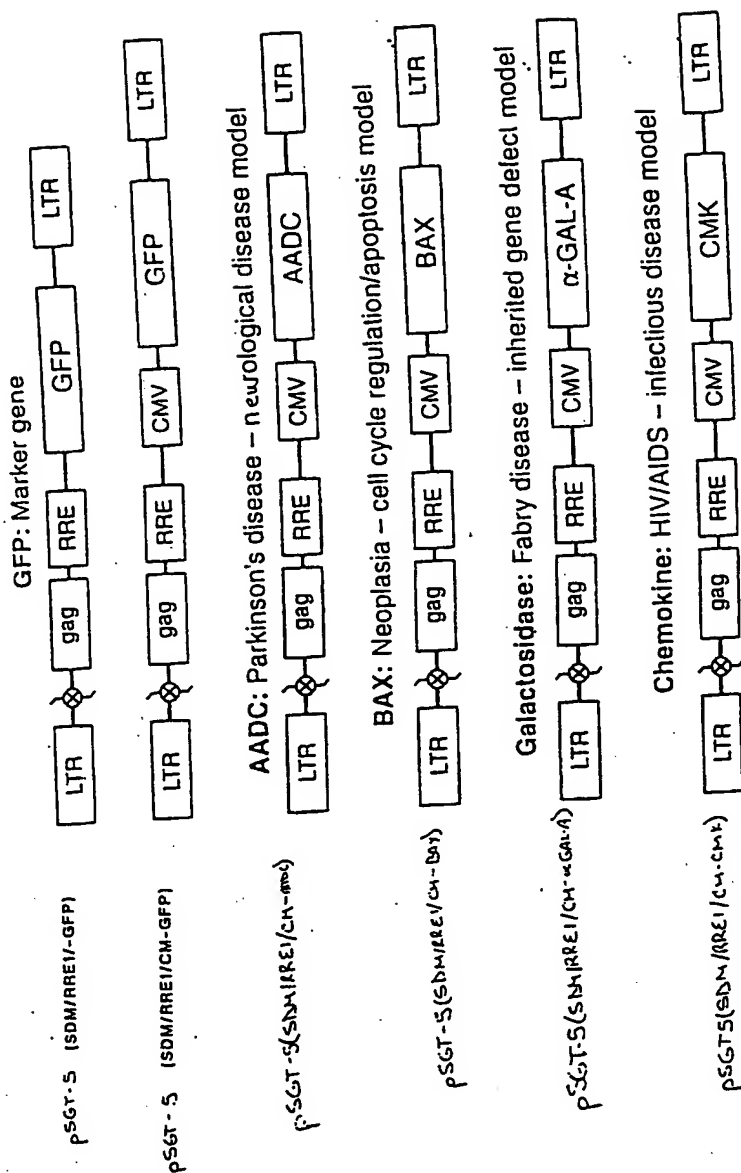


FIG. 13.

% Vector RNA packaged		
	HIV-2 system pROD(SD36)	HIV-1/VSV system
pSGT-5 (SDM) (HIV-2 vector)	8.3 ± 1.2	9.9 ± 0.8
pHR-CM-LUC (HIV-1 vector)	1.0 ± 0.2	16.3 ± 6.5



FIG. 14
HIV-2 Lentivirus Vectors: Gene Transfer Models



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